

#5

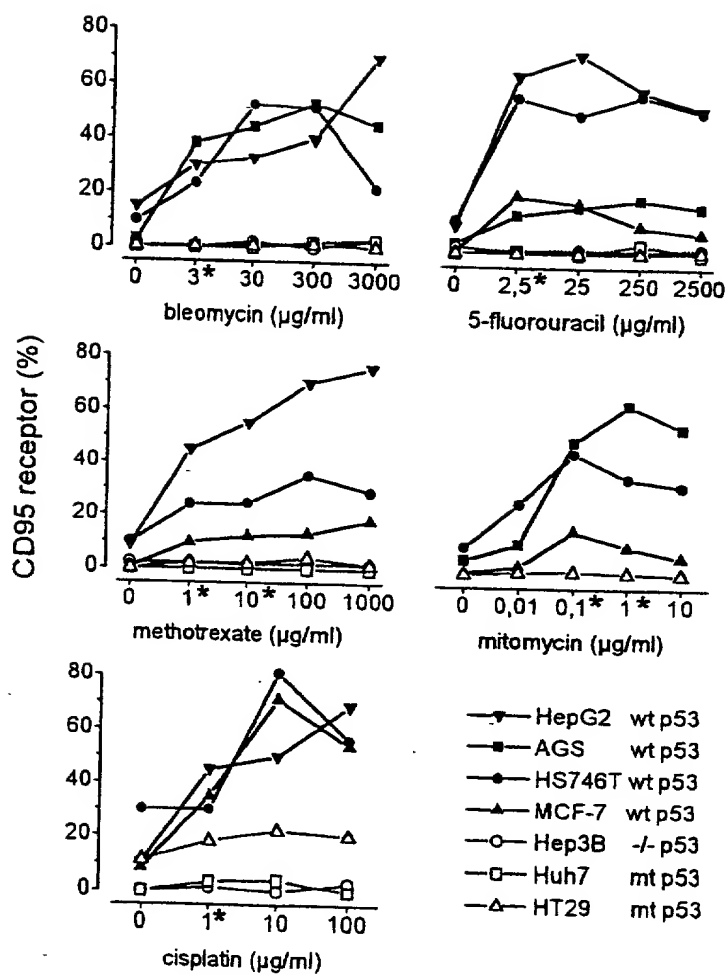


Fig. 1

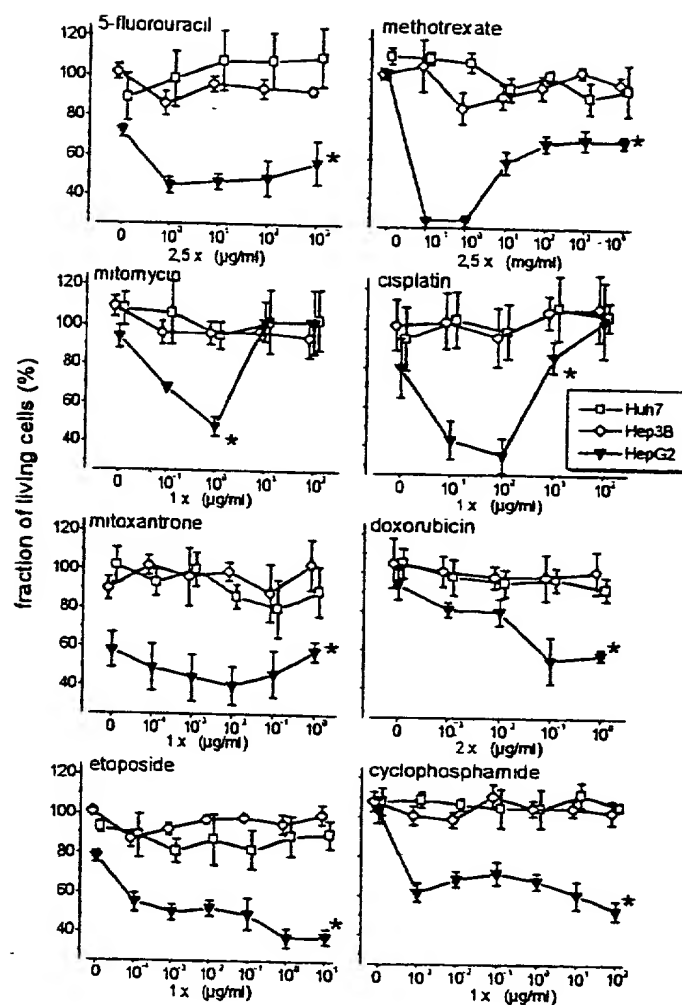


Fig. 2

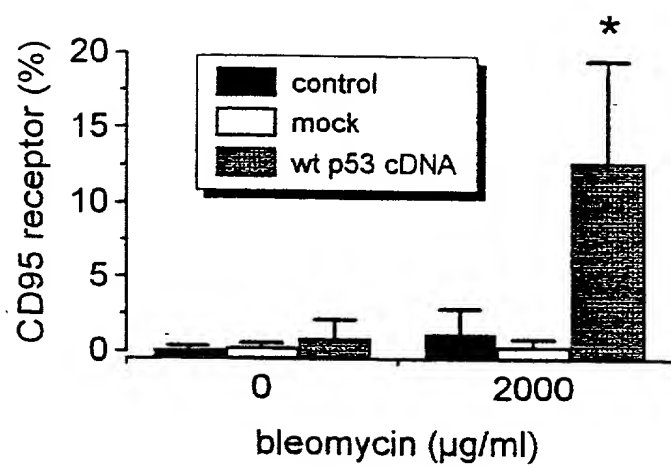


Fig. 3

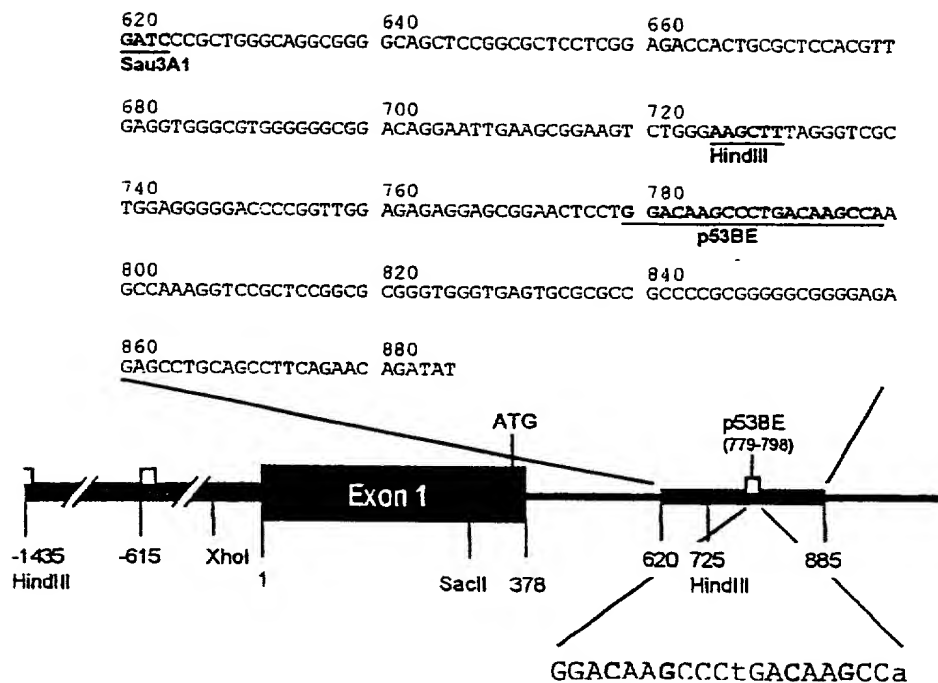


Fig. 4

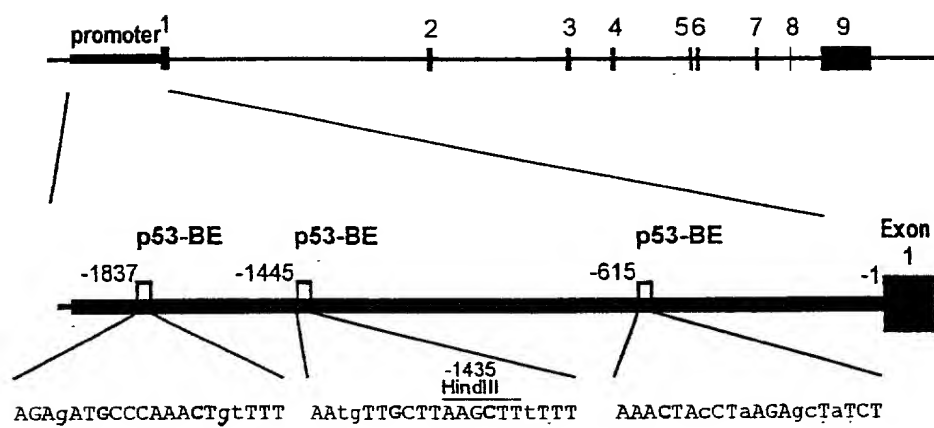


Fig. 5

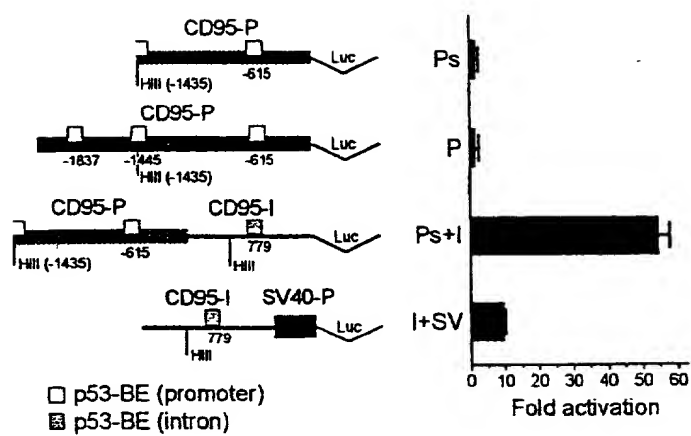


Fig. 6

1 GATCCCGCTGGGCGAGGCGGGGCGAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 60
 CTAGGGCGACCCGCTCCGCCCCGTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA
 61 GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 120
 CTCCACCCGACCCCCCGCTGTCTTAACCTTCGCCTTCAGACCTTCGAAATCCCAGCG
 <---- 4. P53-BE ---->
 (intron)
 121 TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAA 180
 ACCTCCCCCTGGGGCCAACCTCTCTCTCGCCTTGAGGACCTGTTGGGACTGTTTCGGTT
 181 GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGCGGGGAGA 240
 CGGTTTCCAGGCGAGGCCGCGCCACCCACTCACGCGCGGGCGGGGCGCCCCGCCCCCTCT
 241 GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA 300
 CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTT
 301 TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT 360
 ATTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAAAGAAA
 361 CTCGAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT 420
 GAGCTTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA
 421 GTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTA 480
 CAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT
 481 AGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTCTGCCCCTTCTCTTTCTTTCTTTG 540
 TCAGCGACGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAC
 541 CCCTTTCTTAGCTTGCACTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 600
 GGGAAAGAATCGAACGTGAGGGTACCCTAAAGACGAACCAGAGGACGACCCCAACCACC
 601 TACTCGTTCACCCGACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCT 660
 ATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGTTCTTTGAACTCGTCGGA
 661 GTTTTGAAGTCCCTCGCTCAGAAATGCCAGCTTGCAATGGCTAATCAAAGAGACGTG 720
 CAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTCTCTGCAC

Fig. 7

2nd half of the
2.p53-BE
(promoter)

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AGCTTTTTTGGCTACATTTTTTTATTGTAAAG
448 -----+----- 480
TCGAAAAAACCGATGTAAAAAATAAACATTC

TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
481 -----+----- 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTATAATTCAATTCCTTCTAG

CACATATGTGAGTTGCTGGCTTATAATTCACTCAAGAGATACTGATTTTGTCAATTGT
541 -----+----- 600
GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAACAGTTAACA

CCTTCCCTTTTTTCTCTCTCCCTCCCTCCATTCTTCTCCCTTACCTCTCCTTTC
601 -----+----- 660
GGAAAGGGGAAAAAAGAGAGAGGGAGGAAGGTAAGCAAGGAAGGAATGGAGAGGAAAG

CTTCCCTCACACCCCTTTTCCTTCTCTTTTACATTTTTTTATTAAATGAACTTTTC
661 -----+----- 720
GAAGGGAGTGTGGGGAAGGAAGGAAGAAATGTAAAAAATAAATTTACTTGAAAAG

ATTTTGGATAGTTTTAGGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA
721 -----+----- 780
TAAAACCTTATCAAAATCCTAAAGTTTTTAACGTCCTATTATGTCTCTTACGGGTAT

TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
781 -----+----- 840
ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGT

GGCTGGCACGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAGGTGGAACAGAG
841 -----+----- 900
CCGACCGTGCGGGTCCAGAAGGAGTACCGTGATTGTGAGATGACTTTCCACCTTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAAGTGACAGATGCAAAACACAGG
901 -----+----- 960
TGTTCCGATAGTTGTGGATGTTCTGACCACCATTCACGTCAGTGTCTACGTTTGTGTCC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAACAGGCTCCA
991 -----+----- 1020
CACTACCTTTCGGGAGTCTCCCATTTGGATCTAAACTCCCGGGTTTGTCCGAGGT

GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
1021 -----+----- 1080
CTTCTTTACAGTTGACTCTCTTCGGACTTCCTACTTGTCAACCGATTGCTTCCCAAT

```

Fig. 8A

TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
 1081 -----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCCAACCTTAGATTAACCCCTTCCCTCTCTCCAACGTCTCACTCCA

GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
 1141 -----+-----+-----+-----+-----+ 1200
 CGTCTCGAACCACCTGCTACGGTTTCTTATGACTTTGGAAATCACACAGGTCAGACCTT

CTGCATCCAAATTCAGGTTCACTAATGATGTCATTATCCAAACATACCTTCTGTAAAT
 1201 -----+-----+-----+-----+-----+ 1260
 GACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

←--- 3.p53-BE ---→
 (promoter)

CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
 1261 -----+-----+-----+-----+-----+ 1320
 GTACGATTGTGGAATCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCA

TCACCAGAGCACGAAAGATTACAAGATTTTTTTTAAAGAAAATTGGCCAGGAAATAAT
 1321 -----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCTTTATTA

GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTTG
 1381 -----+-----+-----+-----+-----+ 1440
 CTCATTGCTTCCTGTCTTCATTAAACATTACAAATTATATCGACCCCGATACGCTAAAC

GCTTAAGTTGTAGCTTTGTTTTCTCTTGAGAAATAAAAACTAAGGGGCCCTCCCTTTT
 1441 -----+-----+-----+-----+-----+ 1500
 CGAATTCAACAATCGAAACAAAGGAGAACTCTTTATTTTGTATCCCGGGAGGAAAA

CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
 1501 -----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCGCAG
 1561 -----+-----+-----+-----+-----+ 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCCGGTCAGTTTACGGGGCGTTC

TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
 1621 -----+-----+-----+-----+-----+ 1680
 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGAGC

GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCAGGTTGAACTACAGCAGAA
 1681 -----+-----+-----+-----+-----+ 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAACCTTGATGTCGTCTT

GCCTTTAGAAAGGGCAGGAGGCCGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC
 1741 -----+-----+-----+-----+-----+ 1800
 CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTGC

CACTGCAGGAACGCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCC
 1801 -----+-----+-----+-----+-----+ 1860
 GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG

TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
 1861 -----+-----+-----+-----+-----+ 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGTTCAACGACTTAGTTACCTCG

Fig. 8B

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CCTCCCCAACCCGGGGCTTCCCCAGCGAGGCTTCTTCCCATCCTCCTGACCACCGGGG
1921 -----+-----+-----+-----+-----+ 1980
GGAGGGGTGGGCCCCGAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
1981 -----+-----+-----+-----+-----+ 2040
AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA

CTGGGGAGTGAGGGAAGCGGTTTACGAGTGAAGTGGCTGGAGCCTCAGGGGCGGGCACTG
2041 -----+-----+-----+-----+-----+ 2100
GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCGCCCGTGAC

GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGTGCCTCTTCTCCCGC
2101 -----+-----+-----+-----+-----+ 2160
CGTGCCCTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCCTCGACGGAGAAGAGGGCG

GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCGGTGCACCTTAAGCTTTA
2161 -----+-----+-----+-----+-----+ 2220
CCTGTACATGTCTCGAGCTCTTCATGATCACCAGGTGCACCCGGCACGTGGAATTCGAAAT

                                     ←---4.p53-BE-
                                     (intron)

GGGTCGCTGGAGGGGGACCCCGTTGGAGAGAGGAGCGGAACCTCTCGACAAGCCCTGAC
2221 -----+-----+-----+-----+-----+ 2280
CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG

-----→

AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC
2281 -----+-----+-----+-----+-----+ 2340
TTCCGTTTCGGTTTCCAGGCGAGGCGCGCCACCCACTCAGCGCGGGCGGGCGCCCCCG

GGGAGAGAGCCTGCAGCCTTCAGAACAGATATGCTCATTCTTGGCAGTTCTCAGACG
2341 -----+-----+-----+-----+-----+ 2400
CCCCCTCTCTCGGACGTCCGGAAGTCTTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC

TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
2401 -----+-----+-----+-----+-----+ 2460
ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA

TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
2461 -----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

TTTTATTGTACACAGAAAAGGAACTGCCTTGTCTCCCTTCGGGAATTCTCTCTTTAA
2521 -----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT

GACTGTAAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTGTCTTCTGCTTCTCTTTCT
2581 -----+-----+-----+-----+-----+ 2640
CTGACATTTCAGCGACGACTCACCRAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

TCTTTTGCCCTTTCTTAGCTTGAAGTCCCATGGTGATTTCTGCTTGGTCTCCTGTGGGG
2641 -----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAGAATCGAACGTGAGGGTACCCTAAAGACGAACAGAGGACGACCCC

```

Fig. 8C

TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
 2701 -----+-----+-----+-----+-----+ 2760
 AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGGGATAATAACCGGTTCTTTGAACT

 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
 2761 -----+-----+-----+-----+-----+ 2820
 CGTCGGACAAAACCTTTTCAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

 AGACGTG
 2821 ----- 2827
 TCTGCAC

Fig. 8D

<---- 1.p53-BE --

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1  TGAGGACTCTCAGGAATATGCTGGTAAAAATAAAATAACCTTTAGAGATGCCCAAACGT
  -----+-----+-----+-----+-----+-----+
60  ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTGACA
  -----+-----+-----+-----+-----+-----+

-->

61  TTTCCCCAGAACACCAGCATTATTAGGTGTTCAATCAATAGATTCTTCAAAGGATTCCA
  -----+-----+-----+-----+-----+-----+
120  AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCTAAGGT
  -----+-----+-----+-----+-----+-----+

121  AAGGCCAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCTTTGACATTAGCATAC
  -----+-----+-----+-----+-----+-----+
180  TTCCGTTTCTTCAAACCCCTTGTATATATATTAATGGGTGGGAACTGTAATCGTATG
  -----+-----+-----+-----+-----+-----+

181  TAAGGGCCCTGAGAAGTTTGGATTAAGAAAGTTTCAAATTAAGTAACCCAGAATTTT
  -----+-----+-----+-----+-----+-----+
240  ATTCCCGGGACTCTTCAAACCTAATCTTTCAAAGTTTAATTTCAATGGGTCTTAAAA
  -----+-----+-----+-----+-----+-----+

241  CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT
  -----+-----+-----+-----+-----+-----+
300  GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
  -----+-----+-----+-----+-----+-----+

301  GAACCTGAGGATAATTAGACGTACGTGGGTAGAGGTAGGGGAAGGGGGTATGGCATAGA
  -----+-----+-----+-----+-----+-----+
360  CTTGAACCTCTATTAATCTGCATGCACCCATCTCCCATCCCCTCCCCCATACCGTATCT
  -----+-----+-----+-----+-----+-----+

361  AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA
  -----+-----+-----+-----+-----+-----+
420  TTCTCGTCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT
  -----+-----+-----+-----+-----+-----+

<---- 2.p53-BE ---->

421  ACTAACCATCTTTGCCAATGTGCTTAAGCTTTTTTGGCTACATTTTTTTTATTTGTAAG
  -----+-----+-----+-----+-----+-----+
480  TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTTT
  -----+-----+-----+-----+-----+-----+

481  TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
  -----+-----+-----+-----+-----+-----+
540  ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTATAATTCATTCCTTCTAG
  -----+-----+-----+-----+-----+-----+

541  CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
  -----+-----+-----+-----+-----+-----+
600  GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
  -----+-----+-----+-----+-----+-----+

601  CCTTTCCCCTTTTTTTCTCTCTTCCCTCCTTCCATTCCCTTCTTCCCTTACCTCTCCTTTT
  -----+-----+-----+-----+-----+-----+
660  GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAAG
  -----+-----+-----+-----+-----+-----+

```

Fig. 9A

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661  CTTCCTCACACCCCTTTCTCTCCTCTTTTACATTTTTTTATTAAATGAACTTTTC
-----+-----+-----+-----+-----+-----+-----+
720  GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTACTTGAAAAG

721  ATTTTGAATAGTTTTAGGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA
-----+-----+-----+-----+-----+-----+-----+
780  TAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

781  TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
-----+-----+-----+-----+-----+-----+-----+
840  ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

841  GGCTGGCAGCGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
-----+-----+-----+-----+-----+-----+-----+
900  CCGACCGTGGCGGTCCCGAAGGAGTACCGTGATTGTCAGATGACTTTCCACCTTGTCTC

901  ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
-----+-----+-----+-----+-----+-----+-----+
960  TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACGTCACGTGCTACGTTTTGTGTCC

991  GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAAACAGGCTCCA
-----+-----+-----+-----+-----+-----+-----+
1020  CACTACCTTTCCGGAGTCTCCCATTTGGATTGGATCTAAACTCCCGGTTTGTCCGAGGT

1021  GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
-----+-----+-----+-----+-----+-----+-----+
1080  CTCTTTTACAGTTGACTCTCCTTCGGACTTCCTACTTGTCACCCGATTCTGTTTCCCAAT

1081  TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
-----+-----+-----+-----+-----+-----+-----+
1140  AATTACACAATAATTACCCAATTAGATTAAACCTTCCCTCTCTCCAACGTCTCACTCCA

1141  GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
-----+-----+-----+-----+-----+-----+-----+
1200  CGTCTCGAACCACCTGTCTACGGTTTCTTATGACTTTGGAAATCACACAGGTGAGACCTT

1201  CTGCATCCAAATTCAGGTTTCAATGATGTCTATTATCCAAACATACCTTCTGTAAATTT
-----+-----+-----+-----+-----+-----+-----+
1260  GACGTAGGTTTAAAGTCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

<--- 3.p53-BE --->

1261  CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
-----+-----+-----+-----+-----+-----+-----+
1320  GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCAAC

1321  TCACCAGAGCACGAAAGAAATTACAAGATTTTTTTTTAAAGAAAATTGCCAGGAAATAAT
-----+-----+-----+-----+-----+-----+-----+
1380  AGTGGTCTCGTGCTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCCTTTATTA

1381  GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAAATAGCTGGGGCTATGCGATTTG
-----+-----+-----+-----+-----+-----+-----+
1440  CTCATTGCTTCCTGTCCTTCATTAACTTACAAATTATATCGACCCCGATACGCTAAAC

1441  GCTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTT
-----+-----+-----+-----+-----+-----+-----+
1500  CGAATTCAACAATCGAAACAAAAGGAGAACTCTTTATTTTGATTCCCGGGAGGGAAAAA

1501  CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
-----+-----+-----+-----+-----+-----+-----+
1560  GTCTCGGGATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

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Fig. 9B


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TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
2401 -----+-----+-----+-----+-----+ 2460
ATCCTTTATTAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGA

TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTACCGTT
2461 -----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

TTTTATTGTACACAGAAAAGGAACTGCCTTGTCTCCCTTCGGGAATTCTCTCTTTAA
2521 -----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT

GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTGTCTGCTGCTTCTCTTTCT
2581 -----+-----+-----+-----+-----+ 2640
CTGACATTGACGACGGACTCACCAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG
2641 -----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAAGAATCGAACGTGAGGGTACCCTAAAGACGAACCAGAGGACGACCCC

TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
2701 -----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT

GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAG
2761 -----+-----+-----+-----+-----+ 2820
CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGCTACCGATTAGTTTC

AGACGTG
2821 ----- 2827
TCTGCAC

```

Fig. 9D

<---- 1.p53-BE ---->
(promoter)

1 TGAGGACTCTCAGGAATATGCTGGTAAAAATAAAATAACCTTTAGAGATGCCCAAACGTG 60
 ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTTGACA
 -->

61 TTCCCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTTCAAAGGATTCCA 120
 AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTATCTAAGAAGTTTCTTAAGGT
 121 AAGGCCAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCCTTTGACATTAGCATA 180
 TTCCGTTTCTTCAAACCCCTTGTATATATATTAATGGGTGGGAACTGTAATCGTATG
 181 TAAGGGCCCTGAGAAGTTTGGATTAAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT 240
 ATTCCCGGGACTCTTCAAACCTAATTCTTCAAAGTTAATTTCAATTGGGTCTTAAAA
 241 CTAAGATTATTTGACCATGAACATATGTCTCCCCACAAGCAGATATTCCTATCTCCTT 300
 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
 301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGTAGGGGAAGGGGGTATGGCATAGA 360
 CTTGAACTCCTATTATCTGCATGCACCCATCTCCCATCCCCCTCCCCCATACCGTATCT
 361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA 420
 TTCTCGTCTGGAAACCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->
(promoter)

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTGTAAAG 480
 TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTC
 481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
 ATTCAAATTATTAGTGAGTAGAGTGACCGATATTACTATTCTAATTCATTCTTCTAG
 541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGTACTGATTTTGTCAATTGT 600
 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
 601 CCTTTCCCTTTTTTCTCTCTTCCCTCCTTCCATTCTTCTTCCCTTACCTCTCCTTTC 660
 CGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAG
 661 CTTCCCTCACACCCCTTTTCTTCTTCTTTTACATTTTTTTATTTAAATGAACCTTTTC 720
 GAAGGGAGTGTGGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTTACTTGAAAAG
 721 ATTTTGAATAGTTTGTAGGATTTCAAATAATTTGCAGAGATAATACAGAGAATGCCCAT 780
 TAAACCTTATCAAATCCTAAAGTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

Fig. 10A


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      TACCATCCTCCTTATCCCACTTCTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
      ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

      GGCTGGCAGCCCCAGGGTCTTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
      CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTTCACCTTGTCTC

      ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
      TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACAGTCACTGTCTACGTTTGTGTCC

      GTGATGGAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCCAACAGGCTCCAG
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
      CACTACCTTTCGGGAGTCTCTCCATTGGATTGGATCTAACTCCCGGGTTGTCCGAGGTC

      AAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGTTAT
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
      TTCTTTTACAGTTGACTCTCCTTCGACTTCCTACTTGTACCCGATTGCTTTCCCAATA

      TAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGTTGCAGAGTGAGGTG
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
      ATTACACAATAATTACCCAATTAGATTAACCCCTCCCTCTCTCCAACGTCTCACTCCAC

      CAGAGCTTGGTGGCAGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAAC
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
      GTCTCGAACCACTGCTACGGTTCTTATGACTTTGGAATCACACAGGTCAGACCTTG

      TGCATCCAAATTCAGGTTCAAGTAATGATGTCAATTATCCAAACATACCTTCTGTAAATTC
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
      ACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAAG

      <---- 3.p53-BE ---->
      (promoter)

      ATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGAAGTGTGTT
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
      TACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTGTGCACAA

      CACCAGAGCACGAAAGAATTACAAGATTTTTTTTTAAAGAAAATTGGCCAGGAAATAATG
1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380
      GTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCCTTTATTAC

      AGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGGGGCTATGCGATTTGG
1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
      TCATTGCTTCCTGTCCTTCATTAACACTTACAAATTATATCGACCCCGATACGCTAAACC

      CTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTTC
1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
      GAATTCACAATCGAAACAAAGGAGAACTCTTTATTTTGAATCCCCGGGAGGGAAG

      AGAGCCTTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCAGAAACG
1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
      TCTCGGAATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCTTTGC

      TCTGTGAGCCTCTCATGTTGCAGCCCAACATGGACAGCCCAAGTCAAATGCCCGCAAGT
1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
      AGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTGCGGTGAGTTACGGGGCGTTCA

      CTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGCG
1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680
      GAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACGC

      CTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCAGGTTGAACTACAGCAGAAG
1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740
      GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGTCCTCACTTGATGTCGTCTTC

```

Fig. 10B

CTTTAAAGGGCAGGAGGCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGCC
 1741 -----+-----+-----+-----+-----+ 1800
 GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCGG
 ACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCCT
 1801 -----+-----+-----+-----+-----+ 1860
 TGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA
 CACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC
 1861 -----+-----+-----+-----+-----+ 1920
 GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGACTTAGTTACCTCGG
 CTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCTGACCACCGGGGCT
 1921 -----+-----+-----+-----+-----+ 1980
 GAGGGGTTGGGCCCGCAAGGGGTCGCTCCGAAGGAAGGTTAGGAGGACTGGTGGCCCCGA
 TTTCTGTAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC
 1981 -----+-----+-----+-----+-----+ 2040
 AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGCCACAAGTTTCTGCGAAG
 TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG
 2041 -----+-----+-----+-----+-----+ 2100
 ACCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCGCGTGACC
 CACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGCG
 2101 -----+-----+-----+-----+-----+ 2160
 GTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCGC
 GGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTCACTTCGGAGGATTGTCTCA
 2161 -----+-----+-----+-----+-----+ 2220
 CCAACCACCTGGGCGAGTATGCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT
 ACAACCATGCTGGGCATCTGGACCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG
 2221 -----+-----+-----+-----+-----+ 2280
 TGTTGGTACGACCCGTAGACCTGGGAGGATGGAGACCCTAGGGAGAGGACGGGCCACCC
 AGGCTTACCCCGTCTTAGTCCCGGGATAGGCAAGTGGGGCGGGCGGGGACGCGTGCG
 2281 -----+-----+-----+-----+-----+ 2340
 TCCGAATGGGGCAGAATCAGGGCCCTATCCGTTTACCCCGCCCGCGCCCTGCGCACGC
 GGATTGCGGGCGGACGGCGCACCGGGCACCTGGGAGCGCGGGCTGCTGCGGGAGGCG
 2341 -----+-----+-----+-----+-----+ 2400
 CCTAACGCCGCCGTGCGCGCGTGCGCCCGTGGACCCCTGCGCGCCCGACGACGCCCTCCGC
 TTGGAGACTGGCTCCCGGGGGCTGTTAGGACCTTCCCTCAGGCCCGGGTGCTCAGAACGA
 2401 -----+-----+-----+-----+-----+ 2460
 AACCTCTGACCGAGGGCCCCGACAATCCTGGAAGGGAGTCCGGGCCACGAGCTTGTCT
 TGGAGGACTTGCTTTTCTTGGGCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGG
 2461 -----+-----+-----+-----+-----+ 2520
 ACCTCCTGAACGAAAAGAACCAGGAACCTACGCTTACGACTAGGGCGACCCGTCCGCCCC
 CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA
 2521 -----+-----+-----+-----+-----+ 2580
 GTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCACTCCACCCGACCCCCGCGCT
 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTGGCTGGAGGGGACCCCGGTTGGA
 2581 -----+-----+-----+-----+-----+ 2640
 GTCCTTAACCTTCGCTTCAGACCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT
 <---- 4.p53-BE ---->
 (intron)
 GAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCCAAGGTCGCTCCGGCGC
 2641 -----+-----+-----+-----+-----+ 2700
 CTCTCCTCGCCTTGAGGACCTGTTCCGGACTGTTCCGGTTCCAGGCGAGGCCCGC

Fig. 10C

```

GGGTGGGTGAGTGC GCGCCGCCCGGGGGGGGAGAGCCTACAGCCTTCAGAACA
2701 -----+-----+-----+-----+-----+ 2760
CCCACCCACTCACGCGCGGGCGCCCCCGCCCTCTCTCGGATGTCGGAAGTCTTGT

CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG
2761 -----+-----+-----+-----+-----+ 2820
GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTCAC

GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTTCTCGAAAAAGTTATATGGGGG
2821 -----+-----+-----+-----+-----+ 2880
CAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAGAAAGAGCTTTTCAATATACCCCC

CTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATTGTCACACAGAAAAGGAACTG
2881 -----+-----+-----+-----+-----+ 2940
GACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAACAGTGTGTCTTTTCCTTTGAC

CCTTGCTCCTTCCGGAATTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC
2941 -----+-----+-----+-----+-----+ 3000
GGAACAGAGGGAAGGCCCTTAAGAGAGAAATCTGACATTCAGCGACGGACTCACCAAAG

ATTTTGTGTTGTTTTCTGCCCCTTCTTTCTTTCTTTTGGCCCTTTCTTAGCTTGCACTCC
3001 -----+-----+-----+-----+-----+ 3060
TAAACAAAACAAAAGACGGGAAGAGAAAGAAACGGGAAAGAATCGAACGTGAGG

CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCAACCGCACAGA
3061 -----+-----+-----+-----+-----+ 3120
GTACCACTAAAGACGAACCAGAGGACGCCCAACCACCATGAGCAAGGTTGGCGTGTCT

ACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC
3121 -----+-----+-----+-----+-----+ 3180
TGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTGGACAAAACTTTTCAGGGAGCGAG

AGAAATGCCAGCTTGCAATGGCTAATCAAAG
3181 -----+-----+-----+-----+ 3212
TCTTTACGGTCGAACGTCTACCGATTAGTTTC

```

Fig. 10D

Fig. 11A

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GG AAA AAGCCCTGACAAGCCA
	↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2. p1140 IMII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMII	GG AAA AAGCCCTG AAA AGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2280 (C→A)

3. p1140 IMIII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIII	GG AAAT CCCTG AAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2273 (G→T)
2280 (C→A)
2283 (G→T)

Fig. 11B

4. p1140 IMIV

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIV	GC ACAAGCCCT C ACAAGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2268 (G→T)
2278 (C→A)

Fig. 12A

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG AAAAT CCCTG AAAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2. p1141 1p53

p1141	AGAGATGCCCAAAGTGT
p1141 1p53	AGAGAT T CCCAA AAT GT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTT
p1141 2p53	AATGTT T CTTAAG A TTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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4. p1141 3p53

p1141 AAACTACCTAAGAGCTATCT
p1141 3p53 ACAAACCTAAGAGCTATCT
 ↑ ↑

positions of the mutations (boldface and arrow): 1268 (A→C)
1270 (C→A)

5. p1141 Δ Bgl

p1141 AATAACCTTTTAGAGATGCCCCAAACTGTTTTCCCCAGAACA
p1141ABq1 AATAACCTTTA-----GATCTCCCCAGAACA

6. p1141 ΔSpe

p1141 CATCTTTGCCAATGTTGCTTAAGCTTTTTGGCTACATT

p1141ABg1 CATCTTTGCCA-----CTAGTGGCTACATT

7. p1141 Δ Mph

p1141 AATTCATGCTAAACTACCTAAGAGCTATCTTACCGTTCCAA
 p1141ΔBg1 AATTCATGCTATGCA-----TACCGTTCCAA

Fig. 13A

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
2228 (T→A)

2. p1142 IMIII

p1142	GGACAAGCCCTGACAAGCCA
p1142 IMIII	GG AAA TCCCTG AAA TCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)
2665 (G→T)
2672 (C→A)
2675 (G→T)

3. p1142 ΔBgl

	<---- 1.p53-BE ---->
p1142	AATAACCTTT AGAGATGCCCCAACTGTTTT CCCCAGAACA
p1142ΔBgl	AATAACCTTT A ----- GATCT CCCCAGAACA

4. p1142 ΔSpe

	<---- 2.p53-BE ---->
p1142	CATCTTTGCC AATGTTGCTTAAGCTTTTT TGGCTACATT
p1142ΔBgl	CATCTTTGCC A ----- CTAGT TGGCTACATT

Fig. 13B

5. p1142 ΔMph

```

                                <---- 3.p53-BE ---->
p1142      AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
p1142ΔBg1  AATTCATGCTATGCA-----TACCGTTCCAA
```

TOPPUB-1646660

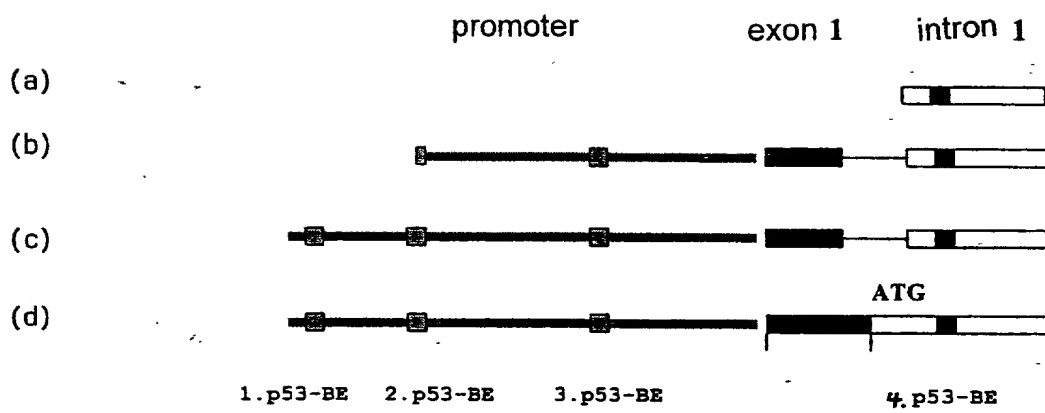


Fig. 14